

# SEQUENCE LISTING

<110> NAKAMURA, Hirofumi  
NAKANE, Akitaka  
KUBOTA, Hidetoshi

<120> B-FRUCTOFURANOSIDASE VARIANTS

<130> 2006\_1464A

<140> US 10/591,751

<141> 2006-09-01

<150> JP 2004-060426

<151> 2004-03-04

<150> PCT/JP2005/003787

<151> 2005-03-04

<160> 18

<170> PatentIn version 3.3

<210> 1

<211> 1905

<212> DNA

<213> Aspergillus niger

<220>

<221> CDS

<222> (1)..(1905)

<400> 1

tca	tac	cac	ctg	gac	acc	acg	gcc	ccg	ccg	ccg	acc	aac	ctc	agc	acc	48
Ser	Tyr	His	Leu	Asp	Thr	Thr	Ala	Pro	Pro	Pro	Thr	Asn	Leu	Ser	Thr	
1				5					10					15		

ctc	ccc	aac	aac	acc	ctc	ttc	cac	gtg	tgg	cgg	ccg	cgc	gcg	cac	atc	96
Leu	Pro	Asn	Asn	Thr	Leu	Phe	His	Val	Trp	Arg	Pro	Arg	Ala	His	Ile	
			20					25					30			

ctg	ccc	gcc	gag	ggc	cag	atc	ggc	gac	ccc	tgc	gcg	cac	tac	acc	gac	144
Leu	Pro	Ala	Glu	Gly	Gln	Ile	Gly	Asp	Pro	Cys	Ala	His	Tyr	Thr	Asp	
		35					40					45				

cca	tcc	acc	ggc	ctc	ttc	cac	gtg	ggg	ttc	ctg	cac	gac	ggg	gac	ggc	192
Pro	Ser	Thr	Gly	Leu	Phe	His	Val	Gly	Phe	Leu	His	Asp	Gly	Asp	Gly	
	50					55					60					

atc	gcg	ggc	gcc	acc	acg	gcc	aac	ctg	gcc	acc	tac	acc	gat	acc	tcc	240
Ile	Ala	Gly	Ala	Thr	Thr	Ala	Asn	Leu	Ala	Thr	Tyr	Thr	Asp	Thr	Ser	
65					70				75						80	

gat	aac	ggg	agc	ttc	ctg	atc	cag	ccg	ggc	ggg	aag	aac	gac	ccc	gtc	288
Asp	Asn	Gly	Ser	Phe	Leu	Ile	Gln	Pro	Gly	Gly	Lys	Asn	Asp	Pro	Val	
				85					90					95		

gcc	gtg	ttc	gac	ggc	gcc	gtc	atc	ccc	gtc	ggc	gtc	aac	aac	acc	ccc	336
Ala	Val	Phe	Asp	Gly	Ala	Val	Ile	Pro	Val	Gly	Val	Asn	Asn	Thr	Pro	
			100					105					110			

acc	tta	ctc	tac	acc	tcc	gtc	tcc	ttc	ctg	ccc	atc	cac	tgg	tcc	atc	384
Thr	Leu	Leu	Tyr	Thr	Ser	Val	Ser	Phe	Leu	Pro	Ile	His	Trp	Ser	Ile	

115					120					125						
ccc Pro	tac Tyr 130	acc Thr	cgc Arg	ggc Gly	agc Ser	gag Glu 135	acg Thr	cag Gln	tcg Ser	ttg Leu	gcc Ala 140	gtc Val	gcg Ala	cgc Arg	gac Asp	432
ggc Gly 145	ggc Gly	cgc Arg	cgc Arg	ttc Phe	gac Asp 150	aag Lys	ctc Leu	gac Asp	cag Gln	ggc Gly 155	ccc Pro	gtc Val	atc Ile	gcc Ala	gac Asp 160	480
cac His	ccc Pro	ttc Phe	gcc Ala	gtc Val 165	gac Asp	gtc Val	acc Thr	gcc Ala	ttc Phe 170	cgc Arg	gat Asp	ccg Pro	ttt Phe	gtc Val 175	ttc Phe	528
cgc Arg	agt Ser	gcc Ala	aag Lys 180	ttg Leu	gat Asp	gtg Val	ctg Leu	ctg Leu 185	tcg Ser	ttg Leu	gat Asp	gag Glu	gag Glu 190	gtg Val	gcg Ala	576
cgg Arg	aat Asn	gag Glu 195	acg Thr	gcc Ala	gtg Val	cag Gln	cag Gln 200	gcc Ala	gtc Val	gat Asp	ggc Gly	tgg Trp 205	acc Thr	gag Glu	aag Lys	624
aac Asn	gcc Ala 210	ccc Pro	tgg Trp	tat Tyr	gtc Val	gcg Ala 215	gtc Val	tct Ser	ggc Gly	ggg Gly	gtg Val 220	cac His	ggc Gly	gtc Val	ggg Gly	672
ccc Pro 225	gcg Ala	cag Gln	ttc Phe	ctc Leu	tac Tyr 230	cgc Arg	cag Gln	aac Asn	ggc Gly	ggg Gly 235	aac Asn	gct Ala	tcc Ser	gag Glu	ttc Phe 240	720
cag Gln	tac Tyr	tgg Trp	gag Glu	tac Tyr 245	ctc Leu	ggg Gly	gag Glu	tgg Trp	tgg Trp 250	cag Gln	gag Glu	gcg Ala	acc Thr	aac Asn 255	tcc Ser	768
agc Ser	tgg Trp	ggc Gly	gac Asp 260	gag Glu	ggc Gly	acc Thr	tgg Trp	gcc Ala 265	ggg Gly	cgc Arg	tgg Trp	ggg Gly	ttc Phe 270	aac Asn	ttc Phe	816
gag Glu	acg Thr	ggg Gly 275	aat Asn	gtg Val	ctc Leu	ttc Phe	ctc Leu 280	acc Thr	gag Glu	gag Glu	ggc Gly	cat His 285	gac Asp	ccc Pro	cag Gln	864
acg Thr	ggc Gly 290	gag Glu	gtg Val	ttc Phe	gtc Val	acc Thr 295	ctc Leu	ggc Gly	acg Thr	gag Glu	ggg Gly 300	tct Ser	ggc Gly	ctg Leu	cca Pro	912
atc Ile 305	gtg Val	ccg Pro	cag Gln	gtc Val	tcc Ser 310	agt Ser	atc Ile	cac His	gat Asp	atg Met 315	ctg Leu	tgg Trp	gcg Ala	gcg Ala	ggt Gly 320	960
gag Glu	gtc Val	ggg Gly	gtg Val	ggc Gly 325	agt Ser	gag Glu	cag Gln	gag Glu	ggt Gly 330	gcc Ala	aag Lys	gtc Val	gag Glu	ttc Phe 335	tcc Ser	1008
ccc Pro	tcc Ser	atg Met	gcc Ala 340	ggg Gly	ttt Phe	ctg Leu	gac Asp	tgg Trp 345	ggg Gly	ttc Phe	agc Ser	gcc Ala	tac Tyr 350	gct Ala	gcg Ala	1056
gcg Ala	ggc Gly	aag Lys 355	gtg Val	ctg Leu	ccg Pro	gcc Ala	agc Ser 360	tcg Ser	gcg Ala	gtg Val	tcg Ser	aag Lys 365	acc Thr	agc Ser	ggc Gly	1104
gtg Val	gag Glu	gtg Val	gat Asp	cgg Arg	tat Tyr	gtc Val	tcg Ser	ttc Phe	gtc Val	tgg Trp	ttg Leu	acg Thr	ggc Gly	gac Asp	cag Gln	1152



625

630

635

<210> 2  
 <211> 635  
 <212> PRT  
 <213> Aspergillus niger

<400> 2

Ser Tyr His Leu Asp Thr Thr Ala Pro Pro Pro Thr Asn Leu Ser Thr  
 1 5 10 15

Leu Pro Asn Asn Thr Leu Phe His Val Trp Arg Pro Arg Ala His Ile  
 20 25 30

Leu Pro Ala Glu Gly Gln Ile Gly Asp Pro Cys Ala His Tyr Thr Asp  
 35 40 45

Pro Ser Thr Gly Leu Phe His Val Gly Phe Leu His Asp Gly Asp Gly  
 50 55 60

Ile Ala Gly Ala Thr Thr Ala Asn Leu Ala Thr Tyr Thr Asp Thr Ser  
 65 70 75 80

Asp Asn Gly Ser Phe Leu Ile Gln Pro Gly Gly Lys Asn Asp Pro Val  
 85 90 95

Ala Val Phe Asp Gly Ala Val Ile Pro Val Gly Val Asn Asn Thr Pro  
 100 105 110

Thr Leu Leu Tyr Thr Ser Val Ser Phe Leu Pro Ile His Trp Ser Ile  
 115 120 125

Pro Tyr Thr Arg Gly Ser Glu Thr Gln Ser Leu Ala Val Ala Arg Asp  
 130 135 140

Gly Gly Arg Arg Phe Asp Lys Leu Asp Gln Gly Pro Val Ile Ala Asp  
 145 150 155 160

His Pro Phe Ala Val Asp Val Thr Ala Phe Arg Asp Pro Phe Val Phe  
 165 170 175

Arg Ser Ala Lys Leu Asp Val Leu Leu Ser Leu Asp Glu Glu Val Ala  
 180 185 190

Arg Asn Glu Thr Ala Val Gln Gln Ala Val Asp Gly Trp Thr Glu Lys  
 195 200 205

Asn Ala Pro Trp Tyr Val Ala Val Ser Gly Gly Val His Gly Val Gly  
 210 215 220

Pro Ala Gln Phe Leu Tyr Arg Gln Asn Gly Gly Asn Ala Ser Glu Phe  
 225 230 235 240  
 Gln Tyr Trp Glu Tyr Leu Gly Glu Trp Trp Gln Glu Ala Thr Asn Ser  
 245 250 255  
 Ser Trp Gly Asp Glu Gly Thr Trp Ala Gly Arg Trp Gly Phe Asn Phe  
 260 265 270  
 Glu Thr Gly Asn Val Leu Phe Leu Thr Glu Glu Gly His Asp Pro Gln  
 275 280 285  
 Thr Gly Glu Val Phe Val Thr Leu Gly Thr Glu Gly Ser Gly Leu Pro  
 290 295 300  
 Ile Val Pro Gln Val Ser Ser Ile His Asp Met Leu Trp Ala Ala Gly  
 305 310 315 320  
 Glu Val Gly Val Gly Ser Glu Gln Glu Gly Ala Lys Val Glu Phe Ser  
 325 330 335  
 Pro Ser Met Ala Gly Phe Leu Asp Trp Gly Phe Ser Ala Tyr Ala Ala  
 340 345 350  
 Ala Gly Lys Val Leu Pro Ala Ser Ser Ala Val Ser Lys Thr Ser Gly  
 355 360 365  
 Val Glu Val Asp Arg Tyr Val Ser Phe Val Trp Leu Thr Gly Asp Gln  
 370 375 380  
 Tyr Glu Gln Ala Asp Gly Phe Pro Thr Ala Gln Gln Gly Trp Thr Gly  
 385 390 395 400  
 Ser Leu Leu Leu Pro Arg Glu Leu Lys Val Gln Thr Val Glu Asn Val  
 405 410 415  
 Val Asp Asn Glu Leu Val Arg Glu Glu Gly Val Ser Trp Val Val Gly  
 420 425 430  
 Glu Ser Asp Asn Gln Thr Ala Arg Leu Arg Thr Leu Gly Ile Thr Ile  
 435 440 445  
 Ala Arg Glu Thr Lys Ala Ala Leu Leu Ala Asn Gly Ser Val Thr Ala  
 450 455 460  
 Glu Glu Asp Arg Thr Leu Gln Thr Ala Ala Val Val Pro Phe Ala Gln  
 465 470 475 480

Ser Pro Ser Ser Lys Phe Phe Val Leu Thr Ala Gln Leu Glu Phe Pro  
 485 490 495  
 Ala Ser Ala Arg Ser Ser Pro Leu Gln Ser Gly Phe Glu Ile Leu Ala  
 500 505 510  
 Ser Glu Leu Glu Arg Thr Ala Ile Tyr Tyr Gln Phe Ser Asn Glu Ser  
 515 520 525  
 Leu Val Val Asp Arg Ser Gln Thr Ser Ala Ala Ala Pro Thr Asn Pro  
 530 535 540  
 Gly Leu Asp Ser Phe Thr Glu Ser Gly Lys Leu Arg Leu Phe Asp Val  
 545 550 555 560  
 Ile Glu Asn Gly Gln Glu Gln Val Glu Thr Leu Asp Leu Thr Val Val  
 565 570 575  
 Val Asp Asn Ala Val Val Glu Val Tyr Ala Asn Gly Arg Phe Ala Leu  
 580 585 590  
 Ser Thr Trp Ala Arg Ser Trp Tyr Asp Asn Ser Thr Gln Ile Arg Phe  
 595 600 605  
 Phe His Asn Gly Glu Gly Glu Val Gln Phe Arg Asn Val Ser Val Ser  
 610 615 620  
 Glu Gly Leu Tyr Asn Ala Trp Pro Glu Arg Asn  
 625 630 635

<210> 3  
 <211> 1809  
 <212> DNA  
 <213> Penicillium roqueforti

<220>  
 <221> CDS  
 <222> (1)..(1809)

<400> 3  
 gtt gat ttc cat acc ccg att gac tat aac tcg gct ccg cca aac ctt 48  
 Val Asp Phe His Thr Pro Ile Asp Tyr Asn Ser Ala Pro Pro Asn Leu  
 1 5 10 15  
 tct acc ctg gca aac gca tct ctt ttc aag aca tgg aga ccc aga gcc 96  
 Ser Thr Leu Ala Asn Ala Ser Leu Phe Lys Thr Trp Arg Pro Arg Ala  
 20 25 30  
 cat ctt ctc cct cca tct ggg aac ata ggc gac ccg tgc ggg cac tat 144  
 His Leu Leu Pro Pro Ser Gly Asn Ile Gly Asp Pro Cys Gly His Tyr  
 35 40 45

acc Thr	gat Asp 50	ccc Pro	aag Lys	act Thr	ggt Gly	ctc Leu 55	ttc Phe	cac His	gtg Val	ggt Gly 60	tgg Trp	ctt Leu	tac Tyr	agt Ser	ggg Gly	192
att Ile 65	tcg Ser	gga Gly	gcg Ala	aca Thr	acc Thr 70	gac Asp	gat Asp	ctc Leu	gtt Val	acc Thr 75	tat Tyr	aaa Lys	gac Asp	ctc Leu	aat Asn 80	240
ccc Pro	gat Asp	gga Gly	gcc Ala	ccg Pro 85	tca Ser	att Ile	gtt Val	gca Ala	gga Gly 90	gga Gly	aag Lys	aac Asn	gac Asp	cct Pro 95	ctt Leu	288
tct Ser	gtc Val	ttc Phe	gat Asp 100	ggc Gly	tcg Ser	gtc Val	att Ile	cca Pro 105	agc Ser	ggt Gly	ata Ile	gac Asp	ggc Gly 110	atg Met	cca Pro	336
act Thr	ctt Leu	ctg Leu 115	tat Tyr	acc Thr	tct Ser	gta Val	tca Ser 120	tac Tyr	ctc Leu	cca Pro	atc Ile	cac His 125	tgg Trp	tcc Ser	atc Ile	384
ccc Pro	tac Tyr 130	acc Thr	cgg Arg	gga Gly	agc Ser	gag Glu 135	aca Thr	caa Gln	tcc Ser	ttg Leu	gcc Ala 140	gtt Val	tcc Ser	tat Tyr	gac Asp	432
ggt Gly 145	ggt Gly	cac His	aac Asn	ttc Phe	acc Thr 150	aag Lys	ctc Leu	aac Asn	caa Gln	ggg Gly 155	ccc Pro	gtg Val	atc Ile	cct Pro	acg Thr 160	480
cct Pro	ccg Pro	ttt Phe	gct Ala	ctc Leu 165	aat Asn	gtc Val	acc Thr	gct Ala	ttc Phe 170	cgt Arg	gac Asp	ccc Pro	tac Tyr	gtt Val 175	ttc Phe	528
caa Gln	agc Ser	cca Pro	att Ile 180	ctg Leu	gac Asp	aaa Lys	tct Ser	gtc Val 185	aat Asn	agt Ser	acc Thr	caa Gln	gga Gly 190	aca Thr	tgg Trp	576
tat Tyr	gtc Val	gcc Ala 195	ata Ile	tct Ser	ggc Gly	ggt Gly	gtc Val 200	cac His	ggt Gly	gtc Val	gga Gly	cct Pro 205	tgt Cys	cag Gln	ttc Phe	624
ctc Leu	tac Tyr 210	cgt Arg	cag Gln	aac Asn	gac Asp	gca Ala 215	gat Asp	ttt Phe	caa Gln	tat Tyr	tgg Trp 220	gaa Glu	tat Tyr	ctc Leu	ggg Gly	672
caa Gln 225	tgg Trp	tgg Trp	aag Lys	gag Glu	ccc Pro 230	ctt Leu	aat Asn	acc Thr	act Thr	tgg Trp 235	gga Gly	aag Lys	ggt Gly	gac Asp	tgg Trp 240	720
gcc Ala	ggg Gly	ggt Gly	tgg Trp	ggc Gly 245	ttc Phe	aac Asn	ttt Phe	gag Glu	gtt Val 250	ggc Gly	aac Asn	gtc Val	ttt Phe	agt Ser 255	ctg Leu	768
aat Asn	gca Ala	gag Glu	ggg Gly 260	tat Tyr	agt Ser	gaa Glu	gac Asp	ggc Gly 265	gag Glu	ata Ile	ttc Phe	ata Ile	acc Thr 270	ctc Leu	ggt Gly	816
gct Ala	gag Glu	ggt Gly 275	tcg Ser	gga Gly	ctt Leu	ccc Pro	atc Ile 280	gtt Val	cct Pro	caa Gln	gtc Val	tcc Ser 285	tct Ser	att Ile	cgc Arg	864
gat Asp	atg Met 290	ctg Leu	tgg Trp	gtg Val	acc Thr	ggc Gly 295	aat Asn	gtc Val	aca Thr	aat Asn	gac Asp 300	ggc Gly	tct Ser	gtc Val	act Thr	912



ttc Phe 305	aag Lys	cca Pro	acc Thr	atg Met	gcg Ala 310	ggt Gly	gtg Val	ctt Leu	gac Asp	tgg Trp 315	ggc Gly	gtg Val	tcg Ser	gca Ala	tat Tyr 320	960
gct Ala	gct Ala	gca Ala	ggc Gly 325	aag Lys	atc Ile	ttg Leu	ccg Pro	gcc Ala	agc Ser 330	tct Ser	cag Gln	gca Ala	tcc Ser	aca Thr 335	aag Lys	1008
agc Ser	ggt Gly	gcc Ala	ccc Pro 340	gat Asp	cgg Arg	ttc Phe	att Ile	tcc Ser 345	tat Tyr	gtc Val	tgg Trp	ctc Leu	act Thr 350	gga Gly	gat Asp	1056
cta Leu	ttc Phe	gag Glu 355	caa Gln	gtg Val	aaa Lys	gga Gly	ttc Phe 360	cct Pro	acc Thr	gct Ala	caa Gln 365	caa Gln	aac Asn	tgg Trp	acc Thr	1104
ggg Gly 370	gcc Ala	ctc Leu	tta Leu	ctg Leu	ccg Pro	cga Arg 375	gag Glu	ctg Leu	aat Asn	gtc Val	cgc Arg 380	act Thr	atc Ile	tct Ser	aac Asn	1152
gtg Val 385	gtg Val	gat Asp	aac Asn	gaa Glu 390	ctt Leu	tcg Ser	cgt Arg	gag Glu	tcc Ser	ttg Leu 395	aca Thr	tcg Ser	tgg Trp	cgc Arg	gtg Val 400	1200
gcc Ala	cgc Arg	gaa Glu	gac Asp	tct Ser 405	ggt Gly	cag Gln	atc Ile	gac Asp	ctt Leu 410	gaa Glu	aca Thr	atg Met	gga Gly	atc Ile 415	tca Ser	1248
att Ile	tcc Ser	agg Arg	gag Glu 420	act Thr	tac Tyr	agc Ser	gct Ala	ctc Leu 425	aca Thr	tcc Ser	ggc Gly	tca Ser	tct Ser 430	ttt Phe	gtc Val	1296
gag Glu	tct Ser	ggt Gly 435	aaa Lys	acg Thr	ttg Leu	tcg Ser	aat Asn 440	gct Ala	gga Gly	gca Ala	gtg Val	ccc Pro 445	ttc Phe	aat Asn	acc Thr	1344
tca Ser 450	ccc Pro	tca Ser	agc Ser	aag Lys	ttc Phe	ttc Phe 455	gtg Val	ctg Leu	aca Thr	gca Ala 460	aat Asn	ata Ile	tct Ser	ttc Phe	ccg Pro	1392
acc Thr 465	tct Ser	gcc Ala	cgt Arg	gac Asp	tct Ser 470	ggc Gly	atc Ile	cag Gln	gct Ala	ggt Gly 475	ttc Phe	cag Gln	gtt Val	tta Leu	tcc Ser 480	1440
tct Ser	agt Ser	ctt Leu	gag Glu 485	tct Ser	aca Thr	act Thr	atc Ile	tac Tyr 490	tac Tyr	caa Gln	ttc Phe	tcc Ser	aac Asn	gag Glu 495	tcc Ser	1488
atc Ile	atc Ile	gtc Val	gac Asp 500	cgc Arg	agc Ser	aac Asn	acg Thr	agt Ser 505	gct Ala	gcg Ala	gcg Ala	aga Arg	aca Thr 510	act Thr	gct Ala	1536
ggg Gly	atc Ile	ctc Leu 515	agt Ser	gat Asp	aac Asn	gag Glu	gcg Ala 520	gga Gly	cgt Arg	ctg Leu	cgc Arg	ctc Leu 525	ttc Phe	gac Asp	gtg Val	1584
ttg Leu	cga Arg 530	aat Asn	gga Gly	aaa Lys	gaa Glu	cag Gln 535	gtt Val	gaa Glu	act Thr	ttg Leu	gag Glu 540	ctc Leu	act Thr	atc Ile	gtg Val	1632
gtg Val 545	gat Asp	aat Asn	agt Ser	gta Val 550	ctg Leu	gaa Glu	gta Val	tat Tyr	gcc Ala	aat Asn 555	gga Gly	cgc Arg	ttt Phe	gct Ala	cta Leu 560	1680



ggc act tgg gct cgg tct tgg tac gcc aac tcg act aaa att aac ttc	1728
Gly Thr Trp Ala Arg Ser Trp Tyr Ala Asn Ser Thr Lys Ile Asn Phe	
	565 570 575
ttc cat aac ggc gtg gga gaa gcg aca ttc gaa gat gtg acg gtc ttt	1776
Phe His Asn Gly Val Gly Glu Ala Thr Phe Glu Asp Val Thr Val Phe	
	580 585 590
gaa gga ctg tat gat gcc tgg cca caa agg aag	1809
Glu Gly Leu Tyr Asp Ala Trp Pro Gln Arg Lys	
	595 600

<210> 4  
 <211> 603  
 <212> PRT  
 <213> Penicillium roqueforti

<400> 4

Val Asp Phe His Thr Pro Ile Asp Tyr Asn Ser Ala Pro Pro Asn Leu	
1 5 10 15	
Ser Thr Leu Ala Asn Ala Ser Leu Phe Lys Thr Trp Arg Pro Arg Ala	
20 25 30	
His Leu Leu Pro Pro Ser Gly Asn Ile Gly Asp Pro Cys Gly His Tyr	
35 40 45	
Thr Asp Pro Lys Thr Gly Leu Phe His Val Gly Trp Leu Tyr Ser Gly	
50 55 60	
Ile Ser Gly Ala Thr Thr Asp Asp Leu Val Thr Tyr Lys Asp Leu Asn	
65 70 75 80	
Pro Asp Gly Ala Pro Ser Ile Val Ala Gly Gly Lys Asn Asp Pro Leu	
85 90 95	
Ser Val Phe Asp Gly Ser Val Ile Pro Ser Gly Ile Asp Gly Met Pro	
100 105 110	
Thr Leu Leu Tyr Thr Ser Val Ser Tyr Leu Pro Ile His Trp Ser Ile	
115 120 125	
Pro Tyr Thr Arg Gly Ser Glu Thr Gln Ser Leu Ala Val Ser Tyr Asp	
130 135 140	
Gly Gly His Asn Phe Thr Lys Leu Asn Gln Gly Pro Val Ile Pro Thr	
145 150 155 160	
Pro Pro Phe Ala Leu Asn Val Thr Ala Phe Arg Asp Pro Tyr Val Phe	
165 170 175	

Gln Ser Pro Ile Leu Asp Lys Ser Val Asn Ser Thr Gln Gly Thr Trp  
 180 185 190  
 Tyr Val Ala Ile Ser Gly Gly Val His Gly Val Gly Pro Cys Gln Phe  
 195 200 205  
 Leu Tyr Arg Gln Asn Asp Ala Asp Phe Gln Tyr Trp Glu Tyr Leu Gly  
 210 215 220  
 Gln Trp Trp Lys Glu Pro Leu Asn Thr Thr Trp Gly Lys Gly Asp Trp  
 225 230 235 240  
 Ala Gly Gly Trp Gly Phe Asn Phe Glu Val Gly Asn Val Phe Ser Leu  
 245 250 255  
 Asn Ala Glu Gly Tyr Ser Glu Asp Gly Glu Ile Phe Ile Thr Leu Gly  
 260 265 270  
 Ala Glu Gly Ser Gly Leu Pro Ile Val Pro Gln Val Ser Ser Ile Arg  
 275 280 285  
 Asp Met Leu Trp Val Thr Gly Asn Val Thr Asn Asp Gly Ser Val Thr  
 290 295 300  
 Phe Lys Pro Thr Met Ala Gly Val Leu Asp Trp Gly Val Ser Ala Tyr  
 305 310 315 320  
 Ala Ala Ala Gly Lys Ile Leu Pro Ala Ser Ser Gln Ala Ser Thr Lys  
 325 330 335  
 Ser Gly Ala Pro Asp Arg Phe Ile Ser Tyr Val Trp Leu Thr Gly Asp  
 340 345 350  
 Leu Phe Glu Gln Val Lys Gly Phe Pro Thr Ala Gln Gln Asn Trp Thr  
 355 360 365  
 Gly Ala Leu Leu Leu Pro Arg Glu Leu Asn Val Arg Thr Ile Ser Asn  
 370 375 380  
 Val Val Asp Asn Glu Leu Ser Arg Glu Ser Leu Thr Ser Trp Arg Val  
 385 390 395 400  
 Ala Arg Glu Asp Ser Gly Gln Ile Asp Leu Glu Thr Met Gly Ile Ser  
 405 410 415  
 Ile Ser Arg Glu Thr Tyr Ser Ala Leu Thr Ser Gly Ser Ser Phe Val  
 420 425 430

Glu Ser Gly Lys Thr Leu Ser Asn Ala Gly Ala Val Pro Phe Asn Thr  
 435 440 445  
 Ser Pro Ser Ser Lys Phe Phe Val Leu Thr Ala Asn Ile Ser Phe Pro  
 450 455 460  
 Thr Ser Ala Arg Asp Ser Gly Ile Gln Ala Gly Phe Gln Val Leu Ser  
 465 470 475 480  
 Ser Ser Leu Glu Ser Thr Thr Ile Tyr Tyr Gln Phe Ser Asn Glu Ser  
 485 490 495  
 Ile Ile Val Asp Arg Ser Asn Thr Ser Ala Ala Ala Arg Thr Thr Ala  
 500 505 510  
 Gly Ile Leu Ser Asp Asn Glu Ala Gly Arg Leu Arg Leu Phe Asp Val  
 515 520 525  
 Leu Arg Asn Gly Lys Glu Gln Val Glu Thr Leu Glu Leu Thr Ile Val  
 530 535 540  
 Val Asp Asn Ser Val Leu Glu Val Tyr Ala Asn Gly Arg Phe Ala Leu  
 545 550 555 560  
 Gly Thr Trp Ala Arg Ser Trp Tyr Ala Asn Ser Thr Lys Ile Asn Phe  
 565 570 575  
 Phe His Asn Gly Val Gly Glu Ala Thr Phe Glu Asp Val Thr Val Phe  
 580 585 590  
 Glu Gly Leu Tyr Asp Ala Trp Pro Gln Arg Lys  
 595 600

<210> 5  
 <211> 1839  
 <212> DNA  
 <213> Scopulariopsis brevicaulis

<220>  
 <221> CDS  
 <222> (1)..(1839)

<400>	5																
caa	cct	acg	tct	ctg	tca	atc	gac	aat	tcc	acg	tat	cct	tct	atc	gac		48
Gln	Pro	Thr	Ser	Leu	Ser	Ile	Asp	Asn	Ser	Thr	Tyr	Pro	Ser	Ile	Asp		
1				5					10					15			
tac	aac	tcc	gcc	cct	cca	aac	ctc	tcg	act	ctt	gcc	aac	aac	agc	ctc		96
Tyr	Asn	Ser	Ala	Pro	Pro	Asn	Leu	Ser	Thr	Leu	Ala	Asn	Asn	Ser	Leu		
			20					25					30				

ttc	gag	aca	tgg	agg	ccg	agg	gca	cac	gtc	ctt	ccg	ccc	cag	aac	cag	144
Phe	Glu	Thr	Trp	Arg	Pro	Arg	Ala	His	Val	Leu	Pro	Pro	Gln	Asn	Gln	
		35					40					45				
atc	ggc	gat	ccg	tgt	atg	cac	tac	acc	gac	ccc	gag	aca	gga	atc	ttc	192
Ile	Gly	Asp	Pro	Cys	Met	His	Tyr	Thr	Asp	Pro	Glu	Thr	Gly	Ile	Phe	
	50					55					60					
cac	gtc	ggc	tgg	ctg	tac	aac	ggc	aat	ggc	gct	tcc	ggc	gcc	acg	acc	240
His	Val	Gly	Trp	Leu	Tyr	Asn	Gly	Asn	Gly	Ala	Ser	Gly	Ala	Thr	Thr	
					70					75					80	
gag	gat	ctc	gtc	acc	tat	cag	gat	ctc	aac	ccc	gac	gga	gcg	cag	atg	288
Glu	Asp	Leu	Val	Thr	Tyr	Gln	Asp	Leu	Asn	Pro	Asp	Gly	Ala	Gln	Met	
				85					90					95		
atc	ctt	ccg	ggc	ggc	gtg	aat	gac	ccc	att	gct	gtc	ttt	gac	ggc	gcg	336
Ile	Leu	Pro	Gly	Gly	Val	Asn	Asp	Pro	Ile	Ala	Val	Phe	Asp	Gly	Ala	
			100					105					110			
gtt	att	ccc	agt	ggc	att	gat	ggg	aaa	ccc	acc	atg	atg	tat	acc	tcg	384
Val	Ile	Pro	Ser	Gly	Ile	Asp	Gly	Lys	Pro	Thr	Met	Met	Tyr	Thr	Ser	
		115					120					125				
gtg	tca	tac	atg	ccc	atc	tcc	tgg	agc	atc	gct	tac	acc	agg	gga	agc	432
Val	Ser	Tyr	Met	Pro	Ile	Ser	Trp	Ser	Ile	Ala	Tyr	Thr	Arg	Gly	Ser	
	130					135					140					
gag	acc	cac	tct	ctc	gca	gtg	tcg	tcc	gac	ggc	ggc	aag	aac	ttc	acc	480
Glu	Thr	His	Ser	Leu	Ala	Val	Ser	Ser	Asp	Gly	Gly	Lys	Asn	Phe	Thr	
					150					155					160	
aag	ctg	gtg	cag	ggc	ccc	gtc	att	cct	tcg	cct	ccc	ttc	ggc	gcc	aac	528
Lys	Leu	Val	Gln	Gly	Pro	Val	Ile	Pro	Ser	Pro	Pro	Phe	Gly	Ala	Asn	
				165					170					175		
gtg	acc	agc	tgg	cgt	gac	ccc	ttc	ctg	ttc	caa	aac	ccc	cag	ttc	gac	576
Val	Thr	Ser	Trp	Arg	Asp	Pro	Phe	Leu	Phe	Gln	Asn	Pro	Gln	Phe	Asp	
			180					185					190			
tct	ctc	ctc	gaa	agc	gag	aac	ggc	acg	tgg	tac	acc	gtt	atc	tct	ggc	624
Ser	Leu	Leu	Glu	Ser	Glu	Asn	Gly	Thr	Trp	Tyr	Thr	Val	Ile	Ser	Gly	
		195					200					205				
ggc	atc	cac	ggc	gac	ggc	ccc	tcc	gcg	ttc	ctc	tac	cgt	cag	cac	gac	672
Gly	Ile	His	Gly	Asp	Gly	Pro	Ser	Ala	Phe	Leu	Tyr	Arg	Gln	His	Asp	
	210					215					220					
ccc	gac	ttc	cag	tac	tgg	gag	tac	ctt	gga	ccg	tgg	tgg	aac	gag	gaa	720
Pro	Asp	Phe	Gln	Tyr	Trp	Glu	Tyr	Leu	Gly	Pro	Trp	Trp	Asn	Glu	Glu	
					230					235					240	
ggg	aac	tcg	acc	tgg	ggc	agc	ggc	gac	tgg	gct	ggc	cgg	tgg	ggc	tac	768
Gly	Asn	Ser	Thr	Trp	Gly	Ser	Gly	Asp	Trp	Ala	Gly	Arg	Trp	Gly	Tyr	
				245					250					255		
aac	ttc	gag	gtc	atc	aac	att	gtc	ggc	ctt	gac	gat	gat	ggc	tac	aac	816
Asn	Phe	Glu	Val	Ile	Asn	Ile	Val	Gly	Leu	Asp	Asp	Asp	Gly	Tyr	Asn	
			260				265						270			
ccc	gac	ggc	gaa	atc	ttt	gcc	acg	gta	ggc	acc	gaa	tgg	tcg	ttt	gac	864
Pro	Asp	Gly	Glu	Ile	Phe	Ala	Thr	Val	Gly	Thr	Glu	Trp	Ser	Phe	Asp	
		275					280					285				

ccc Pro	atc Ile 290	aaa Lys	ccg Pro	cag Gln	gcc Ala	tcg Ser 295	gac Asp	aac Asn	agg Arg	gag Glu	atg Met 300	ctc Leu	tgg Trp	gcc Ala	gcg Ala	912
ggc Gly 305	aac Asn	atg Met	act Thr	ctc Leu	gag Glu 310	gac Asp	ggc Gly	gat Asp	atc Ile	aag Lys 315	ttc Phe	acg Thr	cca Pro	agc Ser	atg Met 320	960
gcg Ala	ggc Gly	tac Tyr	ctc Leu	gac Asp 325	tgg Trp	ggt Gly	cta Leu	tcg Ser	gcg Ala 330	tat Tyr	gcc Ala	gcc Ala	gct Ala	ggc Gly 335	aag Lys	1008
gag Glu	ctg Leu	ccc Pro	gct Ala 340	tct Ser	tca Ser	aag Lys	cct Pro	tcg Ser 345	cag Gln	aag Lys	agc Ser	ggt Gly	gcg Ala 350	ccg Pro	gac Asp	1056
cgg Arg	ttc Phe	gtg Val 355	tcg Ser	tac Tyr	ctg Leu	tgg Trp	ctc Leu 360	acc Thr	ggt Gly	gac Asp	tac Tyr	ttc Phe 365	gag Glu	ggc Gly	cac His	1104
gac Asp	ttc Phe 370	ccc Pro	acc Thr	ccg Pro	cag Gln	cag Gln 375	aat Asn	tgg Trp	acc Thr	ggc Gly	tcg Ser 380	ctt Leu	ttg Leu	ctt Leu	ccg Pro	1152
cgt Arg 385	gag Glu	ctg Leu	agc Ser	gtc Val	ggg Gly 390	acg Thr	att Ile	ccc Pro	aac Asn	gtt Val 395	gtc Val	gac Asp	aac Asn	gag Glu	ctt Leu 400	1200
gct Ala	cgc Arg	gag Glu	acg Thr	ggc Gly 405	tct Ser	tgg Trp	agg Arg	gtt Val	ggc Gly 410	acc Thr	aac Asn	gac Asp	act Thr	ggc Gly 415	gtg Val	1248
ctt Leu	gag Glu	ctg Leu	gtc Val 420	act Thr	ctg Leu	aag Lys	cag Gln	gag Glu 425	att Ile	gct Ala	cgc Arg	gag Glu	acg Thr 430	ctg Leu	gct Ala	1296
gaa Glu	atg Met	acc Thr 435	agc Ser	ggc Gly	aac Asn	tcc Ser	ttc Phe 440	acc Thr	gag Glu	gcg Ala	agc Ser	agg Arg 445	aat Asn	gtc Val	agc Ser	1344
tcg Ser	ccc Pro 450	gga Gly	tct Ser	acc Thr	gcc Ala	ttc Phe 455	cag Gln	cag Gln	tcc Ser	ctg Leu	gat Asp 460	tcc Ser	aag Lys	ttc Phe	ttc Phe	1392
gtc Val 465	ctg Leu	acc Thr	gcc Ala	tcg Ser	ctc Leu 470	tcc Ser	ttc Phe	cct Pro	tcg Ser	tcg Ser 475	gct Ala	cgc Arg	gac Asp	tcc Ser	gac Asp 480	1440
ctc Leu	aag Lys	gct Ala	ggt Gly	ttc Phe 485	gag Glu	atc Ile	ctg Leu	tcg Ser	tcc Ser 490	gag Glu	ttt Phe	gag Glu	tcg Ser	acc Thr 495	acg Thr	1488
gtc Val	tac Tyr	tac Tyr	cag Gln 500	ttt Phe	tcc Ser	aac Asn	gag Glu	tcc Ser 505	atc Ile	atc Ile	att Ile	gac Asp	cgg Arg 510	agc Ser	aac Asn	1536
tcg Ser	agt Ser	gct Ala 515	gcc Ala	gcc Ala	ttg Leu	act Thr	acc Thr 520	gat Asp	gga Gly	atc Ile	gac Asp	acc Thr 525	cgc Arg	aac Asn	gag Glu	1584
ttt Phe	ggc Gly 530	aag Lys	atg Met	cgc Arg	ctg Leu	ttt Phe 535	gat Asp	gtt Val	gtc Val	gag Glu	ggt Gly 540	gac Asp	cag Gln	gag Glu	cgt Arg	1632

atc Ile 545	gag Glu	acg Thr	ctc Leu	gat Asp	ctc Leu 550	act Thr	att Ile	gtg Val	ggt Val	gat Asp 555	aac Asn	tcg Ser	atc Ile	gtt Val	gag Glu 560	1680
ggt Val	cat His	gcc Ala	aac Asn	ggg Gly 565	cga Arg	ttc Phe	gct Ala	ctg Leu	agc Ser 570	act Thr	tgg Trp	gtt Val	cgt Arg	tcg Ser 575	tgg Trp	1728
tac Tyr	gag Glu	tcg Ser	tcc Ser 580	aag Lys	gac Asp	atc Ile	aag Lys	ttc Phe 585	ttc Phe	cac His	gat Asp	ggc Gly	gac Asp 590	agc Ser	acg Thr	1776
ggt Val	cag Gln	ttc Phe 595	tcg Ser	aac Asn	atc Ile	acc Thr	gtc Val 600	tac Tyr	gag Glu	gga Gly	ctg Leu	ttt Phe 605	gac Asp	gcc Ala	tgg Trp	1824
ccg Pro	gag Glu 610	cgg Arg	gcc Ala	agg Arg											1839	

<210> 6  
 <211> 613  
 <212> PRT  
 <213> Scopulariopsis brevicaulis

<400> 6

Gln 1	Pro	Thr	Ser	Leu 5	Ser	Ile	Asp	Asn	Ser 10	Thr	Tyr	Pro	Ser	Ile 15	Asp
Tyr	Asn	Ser	Ala 20	Pro	Pro	Asn	Leu	Ser 25	Thr	Leu	Ala	Asn	Asn 30	Ser	Leu
Phe	Glu	Thr 35	Trp	Arg	Pro	Arg	Ala 40	His	Val	Leu	Pro	Pro 45	Gln	Asn	Gln
Ile 50	Gly	Asp	Pro	Cys	Met	His 55	Tyr	Thr	Asp	Pro	Glu 60	Thr	Gly	Ile	Phe
His 65	Val	Gly	Trp	Leu	Tyr 70	Asn	Gly	Asn	Gly	Ala 75	Ser	Gly	Ala	Thr	Thr 80
Glu	Asp	Leu	Val 85	Thr	Tyr	Gln	Asp	Leu	Asn 90	Pro	Asp	Gly	Ala	Gln 95	Met
Ile	Leu	Pro	Gly 100	Gly	Val	Asn	Asp	Pro 105	Ile	Ala	Val	Phe	Asp 110	Gly	Ala
Val	Ile	Pro 115	Ser	Gly	Ile	Asp	Gly 120	Lys	Pro	Thr	Met	Met 125	Tyr	Thr	Ser
Val 130	Ser	Tyr	Met	Pro	Ile	Ser 135	Trp	Ser	Ile	Ala	Tyr 140	Thr	Arg	Gly	Ser

Glu Thr His Ser Leu Ala Val Ser Ser Asp Gly Gly Lys Asn Phe Thr  
 145 150 155 160  
 Lys Leu Val Gln Gly Pro Val Ile Pro Ser Pro Pro Phe Gly Ala Asn  
 165 170 175  
 Val Thr Ser Trp Arg Asp Pro Phe Leu Phe Gln Asn Pro Gln Phe Asp  
 180 185 190  
 Ser Leu Leu Glu Ser Glu Asn Gly Thr Trp Tyr Thr Val Ile Ser Gly  
 195 200 205  
 Gly Ile His Gly Asp Gly Pro Ser Ala Phe Leu Tyr Arg Gln His Asp  
 210 215 220  
 Pro Asp Phe Gln Tyr Trp Glu Tyr Leu Gly Pro Trp Trp Asn Glu Glu  
 225 230 235 240  
 Gly Asn Ser Thr Trp Gly Ser Gly Asp Trp Ala Gly Arg Trp Gly Tyr  
 245 250 255  
 Asn Phe Glu Val Ile Asn Ile Val Gly Leu Asp Asp Asp Gly Tyr Asn  
 260 265 270  
 Pro Asp Gly Glu Ile Phe Ala Thr Val Gly Thr Glu Trp Ser Phe Asp  
 275 280 285  
 Pro Ile Lys Pro Gln Ala Ser Asp Asn Arg Glu Met Leu Trp Ala Ala  
 290 295 300  
 Gly Asn Met Thr Leu Glu Asp Gly Asp Ile Lys Phe Thr Pro Ser Met  
 305 310 315 320  
 Ala Gly Tyr Leu Asp Trp Gly Leu Ser Ala Tyr Ala Ala Ala Gly Lys  
 325 330 335  
 Glu Leu Pro Ala Ser Ser Lys Pro Ser Gln Lys Ser Gly Ala Pro Asp  
 340 345 350  
 Arg Phe Val Ser Tyr Leu Trp Leu Thr Gly Asp Tyr Phe Glu Gly His  
 355 360 365  
 Asp Phe Pro Thr Pro Gln Gln Asn Trp Thr Gly Ser Leu Leu Leu Pro  
 370 375 380  
 Arg Glu Leu Ser Val Gly Thr Ile Pro Asn Val Val Asp Asn Glu Leu  
 385 390 395 400



Ala Arg Glu Thr Gly Ser Trp Arg Val Gly Thr Asn Asp Thr Gly Val  
405 410 415

Leu Glu Leu Val Thr Leu Lys Gln Glu Ile Ala Arg Glu Thr Leu Ala  
420 425 430

Glu Met Thr Ser Gly Asn Ser Phe Thr Glu Ala Ser Arg Asn Val Ser  
435 440 445

Ser Pro Gly Ser Thr Ala Phe Gln Gln Ser Leu Asp Ser Lys Phe Phe  
450 455 460

Val Leu Thr Ala Ser Leu Ser Phe Pro Ser Ser Ala Arg Asp Ser Asp  
465 470 475 480

Leu Lys Ala Gly Phe Glu Ile Leu Ser Ser Glu Phe Glu Ser Thr Thr  
485 490 495

Val Tyr Tyr Gln Phe Ser Asn Glu Ser Ile Ile Ile Asp Arg Ser Asn  
500 505 510

Ser Ser Ala Ala Ala Leu Thr Thr Asp Gly Ile Asp Thr Arg Asn Glu  
515 520 525

Phe Gly Lys Met Arg Leu Phe Asp Val Val Glu Gly Asp Gln Glu Arg  
530 535 540

Ile Glu Thr Leu Asp Leu Thr Ile Val Val Asp Asn Ser Ile Val Glu  
545 550 555 560

Val His Ala Asn Gly Arg Phe Ala Leu Ser Thr Trp Val Arg Ser Trp  
565 570 575

Tyr Glu Ser Ser Lys Asp Ile Lys Phe Phe His Asp Gly Asp Ser Thr  
580 585 590

Val Gln Phe Ser Asn Ile Thr Val Tyr Glu Gly Leu Phe Asp Ala Trp  
595 600 605

Pro Glu Arg Ala Arg  
610

<210> 7  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 7  
gcgaattcat gaagctcacc actacca

27

<210> 8  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 8  
gcggatcccg gtcaatttct ct

22

<210> 9  
<211> 9  
<212> DNA  
<213> Aspergillus niger

<220>  
<221> CDS  
<222> (1)..(9)

<400> 9  
gac gag gac  
Asp Glu Asp  
1

9

<210> 10  
<211> 9  
<212> DNA  
<213> Aspergillus niger

<220>  
<221> CDS  
<222> (1)..(9)

<400> 10  
ttc atg ccc  
Phe Met Pro  
1

9

<210> 11  
<211> 9  
<212> DNA  
<213> Aspergillus niger

<220>  
<221> CDS  
<222> (1)..(9)

<400> 11  
tcc aac ccc  
Ser Asn Pro  
1

9

<210> 12  
<211> 9  
<212> DNA  
<213> Aspergillus niger

<220>  
<221> CDS  
<222> (1)..(9)

<400> 12  
gcc ttc gac  
Ala Phe Asp  
1

9

<210> 13  
<211> 9  
<212> DNA  
<213> Aspergillus niger

<220>  
<221> CDS  
<222> (1)..(9)

<400> 13  
gtg tac ggc  
Val Tyr Gly  
1

9

<210> 14  
<211> 9  
<212> DNA  
<213> Aspergillus niger

<220>  
<221> CDS  
<222> (1)..(9)

<400> 14  
gcc ctg cag  
Ala Leu Gln  
1

9

<210> 15  
<211> 9  
<212> DNA  
<213> Aspergillus niger

<220>  
<221> CDS  
<222> (1)..(9)

<400> 15  
ttt tcg gag  
Phe Ser Glu  
1

9

<210> 16  
<211> 9  
<212> DNA  
<213> Aspergillus niger

<220>  
<221> CDS  
<222> (1)..(9)

<400> 16  
atc gac gac  
Ile Asp Asp  
1

9

<210> 17  
<211> 9  
<212> DNA  
<213> Aspergillus niger

<220>  
<221> CDS  
<222> (1)..(9)

<400> 17  
ttg atg ggc  
Leu Met Gly  
1

9

<210> 18  
<211> 9  
<212> DNA  
<213> Aspergillus niger

<220>  
<221> CDS  
<222> (1)..(9)

<400> 18  
gtc tgc ttg  
Val Cys Leu  
1

9